

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2005, 09:37:08 ; Search time 11131 Seconds
(without alignments)
11583.805 Million cell updates/sec

Title: US-10-039-272-1
Perfect score: 2661
Sequence: 1 cggcacgagggccagagga.....aaaaaaaaaaaaaaaaaaaaa 2661

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	2650	99.6	2662	9	AF322909	AF322909 Homo sapi
2	2547.8	95.7	2669	6	AR018808	AR018808 Sequence
3	2547.8	95.7	2669	6	AR018814	AR018814 Sequence

	4	2547.8	95.7	2669	6	CQ776677	CQ776677 Sequence
	5	2547.8	95.7	2669	6	AX818137	AX818137 Sequence
	6	2547.8	95.7	2669	9	HSNMB	X76534 H.sapiens N
	7	2533.6	95.2	2658	6	CQ727007	CQ727007 Sequence
	8	2522	94.8	2787	9	BC032783	BC032783 Homo sapi
	9	2485	93.4	2683	6	AX358788	AX358788 Sequence
	10	2485	93.4	2683	6	AX362281	AX362281 Sequence
	11	2485	93.4	2683	9	AY359124	AY359124 Homo sapi
	12	1671	62.8	1683	6	AX677738	AX677738 Sequence
	13	1051.2	39.5	2282	10	BC061725	BC061725 Rattus no
	14	1051.2	39.5	2303	6	AR439670	AR439670 Sequence
	15	1051.2	39.5	2303	6	BD062749	BD062749 Modulator
	16	1049.8	39.5	2279	10	AF322054	AF322054 Mus muscu
	17	1049.8	39.5	2299	10	BC026375	BC026375 Mus muscu
	18	1047.8	39.4	2213	6	AR156839	AR156839 Sequence
	19	1047.8	39.4	2213	6	BD269857	BD269857 The poly
	20	1046.4	39.3	2320	10	AF184983	AF184983 Rattus no
	21	1045	39.3	2305	6	CQ777541	CQ777541 Sequence
	22	1045	39.3	2305	10	MMU251685	AJ251685 Mus muscu
	23	1002.6	37.7	169739	9	AC005082	AC005082 Homo sapi
c	24	988.2	37.1	221255	9	AC145883	AC145883 Pan trogl
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	26	673.6	25.3	820	6	CQ427083	CQ427083 Sequence
	27	584.6	22.0	2467	5	CJQNR71	X94144 C.japonica
	28	572	21.5	1690	9	BC011595	BC011595 Homo sapi
	29	568.8	21.4	1593	9	HSA505015	AJ505015 Homo sapi
	30	546.4	20.5	621	9	BT007074	BT007074 Homo sapi
	31	546.4	20.5	621	12	BT007499	BT007499 Synthetic
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	35	545.6	20.5	619	6	BD275711	BD275711 COMPOUNDS
	36	545.6	20.5	619	6	BD275724	BD275724 COMPOUNDS
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	38	545.6	20.5	619	6	AR220509	AR220509 Sequence
	39	545.6	20.5	619	6	AR255490	AR255490 Sequence
	40	545.6	20.5	619	6	AR255503	AR255503 Sequence
	41	545.6	20.5	619	6	AR281060	AR281060 Sequence
	42	545.6	20.5	619	6	AR281073	AR281073 Sequence
	43	545.6	20.5	619	6	AR437851	AR437851 Sequence
	44	545.6	20.5	619	6	AR437864	AR437864 Sequence
	45	545.6	20.5	619	6	AR476387	AR476387 Sequence

ALIGNMENTS

RESULT 1

AF322909

LOCUS AF322909 2662 bp mRNA linear PRI 23-APR-2003
 DEFINITION Homo sapiens transmembrane glycoprotein HGFIN mRNA, complete cds.
 ACCESSION AF322909
 VERSION AF322909.1 GI:11993664
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                1 (bases 1 to 2662)
AUTHORS        Bandari,P.S., Qian,J., Yehia,G., Joshi,D.D., Maloof,P.B.,
                Potian,J., Oh,H.S., Gascon,P., Harrison,J.S. and Rameshwar,P.
TITLE          Hematopoietic growth factor inducible neurokinin-1 type: a
                transmembrane protein that is similar to neurokinin 1 interacts
                with substance P
JOURNAL        Regul. Pept. 111 (1-3), 169-178 (2003)
MEDLINE        22498106
PUBMED         12609765
REFERENCE      2 (bases 1 to 2662)
AUTHORS        Rameshwar,P.
TITLE          Direct Submission
JOURNAL        Submitted (20-NOV-2000) Medicine, UMDNJ-New Jersey Medical School,
                185 South Orange Ave, MSB, Rm. E-579, Newark, NJ 07103, USA
FEATURES
  source        Location/Qualifiers
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                PFPHPHGWRRWNFIYVFHTLGQYFQKLGRCSVRVSVNTANVT LGPQLMEVTVYRRHGR
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                STINYKWSFGDNTGLFVSTNHTVNHTYVLNGTFSLNLTVKAAAPGPCPPPPPPRPSK
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ORIGIN

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Query Match          99.6%; Score 2650; DB 9; Length 2662;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1 CGGCACGAGGGCCCAGAGGAATAAGTTAACCTTGGTGCCTGCGTCCGTGAGAATTCAGCA 60
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Db      1 CGGCACGAGGGCCCAGAGGAATAAGTTAACCTTGGTGCCTGCGTCCGTGAGAATTCAGCA 60

Qy      61 TGGAATGTCTCTACTATTTCCCTGGGATTTCTGCTCCTGGCTGCAAGATTGCCACTTGATG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGGAATGTCTCTACTATTTCCCTGGGATTTCTGCTCCTGGCTGCAAGATTGCCACTTGATG 120

Qy      121 CCGCCAAACGATTTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAGC 180
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Db      121 CCGCCAAACGATTTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAGC 180

Qy      181 ACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAAACTCTACCCAG 240

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Db	181 ACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAACTCTACCCAG	240
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Db	301 TCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTGA	360
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Db	361 TATTCCCTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAAGCTGCA	420
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Db	421 GAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAACCTGGACAGCATGGTCAGAGG	480
Qy	481 ACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAAC	540
Db	481 ACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAAC	540
Qy	541 CTTTTCTCACCACCCCGGATGGAGAAGATGGAATTTTCATCTACGTCTTCCACACACTTG	600
Db	541 CTTTTCTCACCACCCCGGATGGAGAAGATGGAATTTTCATCTACGTCTTCCACACACTTG	600
Qy	601 GTCAGTATTTCCAGAAATTGGGACGATGTTTCAGTGAGAGTTTCTGTGAACACAGCCAATG	660
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Qy	661 TGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATG	720
Db	661 TGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATG	720
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Qy	840 TTATGTTTGATGTCCTGATTTCATGATCCTAGCCACTTCCTCAATTATTCTACCATTAAC	899
Db	841 TTATGTTTGATGTCCTGATTTCATGATCCTAGCCACTTCCTCAATTATTCTACCATTAAC	900
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Db	901 ACAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATACTGTGAATC	960
Qy	960 ACACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCAG	1019
Db	961 ACACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCAG	1020
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Db	1021	GACCTTGTCCGCCACCGCCACCACCACCCAGACCTTCAAAACCCACCCCTTCTTTAGGAC	1080
Qy	1080	CTGCTGGTGACAACCCCTGGAGCTGAGTAGGATTCCCTGATGAAAACGCCAGATTAACA	1139
Db	1081	CTGCTGGTGACAACCCCTGGAGCTGAGTAGGATTCCCTGATGAAAACGCCAGATTAACA	1140
Qy	1140	GATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAGGTTAACATCA	1199
Db	1141	GATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAGGTTAACATCA	1200
Qy	1200	TCCAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTTG	1259
Db	1201	TCCAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTTG	1260
Qy	1260	TCGTGACCTGCCAAGGGAGCATTTCCACGGAGGTCTGTACCATCATTTCTGACCCACCT	1319
Db	1261	TCGTGACCTGCCAAGGGAGCATTTCCACGGAGGTCTGTACCATCATTTCTGACCCACCT	1320
Qy	1320	GCGAGATCACCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGATGTGTCTGCTGA	1379
Db	1321	GCGAGATCACCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGATGTGTCTGCTGA	1380
Qy	1380	CTGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCTGGGGGATG	1439
Db	1381	CTGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCTGGGGGATG	1440
Qy	1440	ACACAAGCCTGGCTCTCACGAGCACCTGATTTCTGTTCCCTGACAGAGACCCAGCCTCGC	1499
Db	1441	ACACAAGCCTGGCTCTCACGAGCACCTGATTTCTGTTCCCTGACAGAGACCCAGCCTCGC	1500
Qy	1500	CTTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACTG	1559
Db	1501	CTTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACTG	1560
Qy	1560	TGATCTCCCTCTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCTG	1619
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Qy	1680	TCCCGGGAACAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCTT	1739
Db	1681	TCCCGGGAACAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCTT	1740
Qy	1740	AAATTTGACCTTGTTTCTGAAGCTCACTTTTCAGTGCCATTGATGTGAGATGTGCTGGA	1799
Db	1741	AAATTTGACCTTGTTTCTGAAGCTCACTTTTCAGTGCCATTGATGTGAGATGTGCTGGA	1800
Qy	1800	GTGGCTATTAACCTTTTTTCTAAAGATTATTGTTAAATAGATATTGTGGTTTGGGGAA	1859
Db	1801	GTGGCTATTAACCTTTTTTCTAAAGATTATTGTTAAATAGATATTGTGGTTTGGGGAA	1860
Qy	1860	GTTGAATTTTTTATAGGTTAAATGTCATTTTAGAGATGGGGAGAGGGATTATACTGCAGG	1919
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Qy	1920	CAGCTTCAGCCATGTTGTGAAACTGATAAAAGCAACTTAGCAAGGCTTCTTTTCATTATT	1979
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Qy	1980	TTTTATGTTTCACTTATAAAGTCTTAGGTAAGTAGTAGGATAGAAACACTGTGTCCCGAG	2039
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Db	2281	CTCTCATAAATGGGTGGGAGTATTTTGGTGACAACCTACTTTGCTTGGCTGAGTGAAGGA	2340
Qy	2340	ATGATATTCATATATTCATTTATTCATGGACATTTAGTTAGTGCTTTTTATATACCAGG	2399
Db	2341	ATGATATTCATATATTCATTTATTCATGGACATTTAGTTAGTGCTTTTTATATACCAGG	2400
Qy	2400	CATGATGCTGAGTGACACTCTTGTGTATATTTCCAAATTTTGTATAGTCGCTGCACATA	2459
Db	2401	CATGATGCTGAGTGACACTCTTGTGTATATTTCCAAATTTTGTATAGTCGCTGCACATA	2460
Qy	2460	TTTGAAATCAAAATATTAAGACTTTCCAAAATTTGGTCCCTGGTTTTTCATGGCAACTT	2519
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Qy	2520	GATCAGTAAGGATTTCCCTCTGTTTGGAACATAAACCATTTACTATATGTTAGACAAGA	2579
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Qy	2580	CATTTTTTTTTTTTCTTCTGAAAAAAATGAGGGAAGAGACAAAAAAAAAAAAAAAAA	2639
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RESULT 2

AR018808

LOCUS

AR018808

2669 bp

DNA

linear

PAT 05-DEC-1998

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Qy	628	GTTTCAGTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAG	687
Db	660	GTTTCAGTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAG	719
Qy	688	TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAGATGTGT	747
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Qy	748	ACGTGGTAACAGATCAGATTCCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATT	807
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Qy	808	CATCCGACGAAACCTTCC-CAAAGATCTCCCCATTATGTTTGATGTCTGATTCATGATC	866
Db	840	CATCCGACGAAACCTTCCCTCAAAGATCTCCCCATTATGTTTGATGTCTGATTCATGATC	899
Qy	867	CTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTG	926
Db	900	CTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTG	959
Qy	927	GCCTGTTTGTTCACCAATCATACTGTGAATCACACGTATGTGCTCAATGGAACCTTCA	986
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Db	1440	 GGACGTACTGTGTGAACCTCACCCCTGGGGGATGACACAAGCCTGGCTCTCACGAGCACCC	1499
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Db	1500	 TGATTTCTGTTCTTGACAGAGACCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGA	1559
Qy	1527	TCTCCGTTGGCTGCTTGGCCATATTTGTCACTGTGATCTCCCTCTTGGTGTACAAAAAC	1586
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Qy	1587	ACAAGGAATACAACCCAATAGAAAAATAGTCCTGGAATGTGGTCAGAAGCAAAGGCCCTGA	1646
Db	1620	 ACAAGGAATACAACCCAATAGAAAAATAGTCCTGGAATGTGGTCAGAAGCAAAGGCCCTGA	1679
Qy	1647	GTGTCTTTCTCAACCGTGCAAAGCCGTGTTCTTCCCGGGAACCAAGGAAAGGATCCGC	1706
Db	1680	 GTGTCTTTCTCAACCGTGCAAAGCCGTGTTCTTCCCGGGAACCAAGGAAAGGATCCGC	1739
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Db	1740	 TACTCAAAAACCAAGAATTTAAAGGAGTTTCTTAAATTTTCGACCTTGTTTCTGAAGCTCA	1799
Qy	1767	CTTTTCAGTGCCATTGATGTGAGATGTGCTGGAGTGGCTATTAACCTTTTTTTCCTAAAG	1826
Db	1800	 CTTTTCAGTGCCATTGATGTGAGATGTGCTGGAGTGGCTATTAACCTTTTTTTCCTAAAG	1859
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Qy	1887	TTTTAGAGATGGGGAGAGGGATTATACTGCAGGCAGCTTCAGCCATGTTGTGAAACTGAT	1946
Db	1920	 TTTTAGAGATGGGGAGAGGGATTATACTGCAGGCAGCTTCAGCCATGTTGTGAAACTGAT	1979
Qy	1947	AAAAGCAACTTAGCAAGGCTTCTTTTCATTATTTTTTATGTTTCACCTATAAAGTCTTAG	2006
Db	1980	 AAAAGCAACTTAGCAAGGCTTCTTTTCATTATTTTTTATGTTTCACCTATAAAGTCTTAG	2039
Qy	2007	GTAAC TAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAGAAGCTACTATTGATTA	2066
Db	2040	 GTAAC TAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAGAAGCTACTATTGATTA	2099
Qy	2067	GAGCCTAACCCAGGTTAACTGCAAGAAGAGGCGGGATACTTTCAGCTTTCATGTAAGTG	2126
Db	2100	 GAGCCTAACCCAGGTTAACTGCAAGAAGAGGCGGGATACTTTCAGCTTTCATGTAAGTG	2159
Qy	2127	TATGCATAAAGCCAATGTAGTCCAGTTTCTAAGATCATGTTCCAAGCTAACTGAATCCCA	2186
Db	2160	 TATGCATAAAGCCAATGTAGTCCAGTTTCTAAGATCATGTTCCAAGCTAACTGAATCCCA	2219
Qy	2187	CTTCAATACACACTCATGAACCTCCTGATGGAACAATAACAGGCCCAAGCCTGTGGTATGA	2246
Db	2220	 CTTCAATACACACTCATGAACCTCCTGATGGAACAATAACAGGCCCAAGCCTGTGGTATGA	2279
Qy	2247	TGTGCACACTTGCTAGACTCAGAAAAAATACTACTCTCATAAATGGGTGGGAGTATTTTG	2306

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Db      2280 TGTGCACACTTGCTAGACTCAGAAAAAATACTACTCTCATAAATGGGTGGGAGTATTTTG 2339
Qy      2307 GTGACAACCTACTTTGCTTGGCTGAGTGAAGGAATGATATTCATATATTCATTTATTCCA 2366
        |||
Db      2340 GTGACAACCTACTTTGCTTGGCTGAGTGAAGGAATGATATTCATATATTCATTTATTCCA 2399
Qy      2367 TGGACATTTAGTTAGTGCTTTTTATATACCAGGCATGATGCTGAGTGACACTCTTGTGTA 2426
        |||
Db      2400 TGGACATTTAGTTAGTGCTTTTTATATACCAGGCATGATGCTGAGTGACACTCTTGTGTA 2459
Qy      2427 TATTTCCAAATTTTTGTATAGTCGCTGCACATATTTGAAATCAAATATTAAGACTTTCC 2486
        |||
Db      2460 TATTTCCAAATTTTTGTATAGTCGCTGCACATATTTGAAATC-ATATATTAAGACTTTCC 2518
Qy      2487 AAAAATTTGGTCCCTGGTTTTTTCATGGCAACTTGATCAGTAAGGATTTCCCCTCTGTTTG 2546
        |||
Db      2519 AAAGATGAGGTCCCTGGTTTTTTCATGGCAACTTGATCAGTAAGGATTTACCTCTGTTTG 2578
Qy      2547 GAACTAAAACCATTTACTATATGTTAGACAAGACATTTTTTTTTTTTCCCTTCCTGAAAAA 2606
        |||
Db      2579 TAACTAAAACCATCTACTATATGTTAGACATGACATTCCTTTTCTCTCCTTCCTGAAAAA 2638
Qy      2607 -AAAATGAGGGAAGAGACAAAAAAAAAAAAA 2636
        |||
Db      2639 TAAAGTGTGGGAAGAGACAAAAAAAAAAAAA 2669

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2005, 08:39:53 ; Search time 1308 Seconds
(without alignments)
12043.143 Million cell updates/sec

Title: US-10-039-272-1
Perfect score: 2661
Sequence: 1 cggcagcagggccagagga.....aaaaaaaaaaaaaaaaaaaaa 2661

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*

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5: geneseqn2001bs:*
6: geneseqn2002as:*
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8: geneseqn2003as:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2661	100.0	2661	6	ABQ78551	Abq78551 Nucleotid
2	2571.2	96.6	2845	12	ADQ22838	Adq22838 Human sof
3	2559.2	96.2	2952	11	ACN89693	Acn89693 Breast ca
4	2547.8	95.7	2669	2	AAT69328	Aat69328 Murine me
5	2547.8	95.7	2669	2	AAT69318	Aat69318 Murine me
6	2547.8	95.7	2669	3	AAC55715	Aac55715 Human NMB
7	2547.8	95.7	2669	6	ABQ88185	Abq88185 Human ost
8	2547.8	95.7	2669	8	ABX76321	Abx76321 Lung canc
9	2547.8	95.7	2669	10	ADL14996	Adl14996 Human NMB
10	2547.8	95.7	2669	11	ADN39723	Adn39723 Cancer/an
11	2547.8	95.7	2669	12	ADJ75111	Adj75111 Marker ge
12	2547.8	95.7	2669	12	ADQ18309	Adq18309 Human sof
13	2547.8	95.7	2669	13	ADR24918	Adr24918 Breast ca
14	2547.8	95.7	2669	13	ADP23126	Adp23126 PRO polyp
15	2547.8	95.7	2669	13	ADR66172	Adr66172 Human pro
16	2547.8	95.7	2669	13	ADR66150	Adr66150 Human pro
17	2531.6	95.1	2666	10	ADJ56363	Adj56363 Human cDN
18	2505.6	94.2	2728	10	ADD78274	Add78274 Human CGD
19	2485	93.4	2683	6	ABK33556	Abk33556 cDNA enco
20	2485	93.4	2683	8	ACA68517	Aca68517 Novel hum
21	2485	93.4	2683	9	ABT44246	Abt44246 Human PRO
22	2485	93.4	2683	9	ABT44529	Abt44529 Human PRO
23	2485	93.4	2683	9	ACD82196	Acd82196 Human sec
24	2485	93.4	2683	9	ABT43902	Abt43902 Human mem
25	2485	93.4	2683	9	ADB83531	Adb83531 Novel hum
26	2485	93.4	2683	9	ADB80637	Adb80637 Novel hum
27	2485	93.4	2683	9	ADB73178	Adb73178 Novel hum
28	2485	93.4	2683	9	ADB78260	Adb78260 Novel hum
29	2485	93.4	2683	10	ADB84908	Adb84908 Human PRO
30	2485	93.4	2683	10	ADB78014	Adb78014 Novel hum
31	2485	93.4	2683	10	ADB87080	Adb87080 Human PRO
32	2485	93.4	2683	10	ADB84662	Adb84662 Human PRO
33	2485	93.4	2683	10	ADB83777	Adb83777 Novel hum
34	2485	93.4	2683	10	ADB72932	Adb72932 Novel hum
35	2485	93.4	2683	10	ADC36770	Adc36770 Human PRO
36	2485	93.4	2683	10	ADC21760	Adc21760 Human PRO

37	2485	93.4	2683	10	ADC49791	Adc49791	Novel	hum
38	2485	93.4	2683	10	ADC48990	Adc48990	Novel	hum
39	2485	93.4	2683	10	ADC49507	Adc49507	Novel	hum
40	2485	93.4	2683	10	ADC47368	Adc47368	Novel	hum
41	2485	93.4	2683	10	ADC47113	Adc47113	Novel	hum
42	2485	93.4	2683	10	ADC77988	Adc77988	Novel	hum
43	2485	93.4	2683	10	ADD06223	Add06223	Novel	hum
44	2485	93.4	2683	10	ADC77742	Adc77742	Novel	hum
45	2485	93.4	2683	10	ADD50705	Add50705	Novel	hum

ALIGNMENTS

RESULT 1

ABQ78551

ID ABQ78551 standard; DNA; 2661 BP.

XX

AC ABQ78551;

XX

DT 25-NOV-2002 (first entry)

XX

DE Nucleotide sequence of human HGFIN.

XX

KW Human; cell differentiation; white blood cell; bone marrow cell;

KW haematopoietic growth factor inducible neurokin-1; HGFIN;

KW progenitor proliferation; acute myeloid leukemia; non-Hodgkin's disease;

KW acute lymphocytic leukemia; chronic myeloid leukemia;

KW chronic lymphocytic leukemia; Hodgkin's disease; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 60. .1741

FT /*tag= a

FT /product= "HGFIN"

FT /transl_except= (825. .826,aa:Leu)

XX

PN WO200262947-A2.

XX

PD 15-AUG-2002.

XX

PF 20-OCT-2001; 2001WO-US050204.

XX

PR 20-OCT-2000; 2000US-0241881P.

XX

PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

XX

PI Pranela R;

XX

DR WPI; 2002-657531/70.

DR P-PSDB; ABB78200.

XX

PT Hematopoietic growth factor inducible neurokin-1 type polypeptide and

PT polynucleotide for treating a disease associated with abnormal bone

PT marrow cell differentiation or proliferation, e.g. leukemia.

XX

PS Claim 2; Page 121-123; 125pp; English.

XX

CC The present sequence encodes human haematopoietic growth factor inducible
CC neurokinin-1 type (HGFIN) polypeptide. HGFIN induces white blood cell
CC differentiation and inhibits progenitor proliferation. HGFIN polypeptides
CC and polynucleotides are useful for treating a disease associated with
CC abnormal bone marrow cell differentiation or proliferation, especially
CC acute myeloid leukemia, acute lymphocytic leukemia, chronic myeloid
CC leukemia, chronic lymphocytic leukemia, Hodgkin's and non-Hodgkin's
CC disease

SQ Sequence 2661 BP; 772 A; 586 C; 587 G; 716 T; 0 U; 0 Other;

Query Match 100.0%; Score 2661; DB 6; Length 2661;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2661; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCACGAGGGCCCAGAGGAATAAGTTAACCTTGGTGCCTGCGTCCGTGAGAATTCAGCA 60

QY 61 TGG AATGTCTCTACTATTTCTG GGGATTTC TGCTCCTGGCTGCAAGATTGCCACTTGATG 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 CCGCCAAACGATTTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAGC 180
| | | | | | | | | | | | | | | | | | | | | | |

Qy 181 ACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAACTCTACCCAG 240
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 241 TGTGGAAGCGGGGAGACATGAGGTGGA AAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGG 300
| | | | | | | | | | | | | | | | | | | | | |

[illegible]

Qy 361 TATTCCCTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAAGCTGCA 420
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 421 GAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAACTGGACAGCATGGTCAGAGG 480

[illegible]

Qy 541 CTTTTCCTCACCACCCGGATGGAGAAGATGGAATTTTCATCTACGTCTTCCACACACTTG 600
|||||

Db 541 CTTTTCCTCACCACCCCGGATGGAGAAGATGGAATTCATCTACGTCTTCCACACACTTG 600

Qy	601	GTCAGTATTTCCAGAAATTGGGACGATGTTTCAGTGAGAGTTTCTGTGAACACAGCCAATG	660
Db	601	GTCAGTATTTCCAGAAATTGGGACGATGTTTCAGTGAGAGTTTCTGTGAACACAGCCAATG	660
Qy	661	TGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATG	720
Db	661	TGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATG	720
Qy	721	TTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTGA	780
Db	721	TTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTGA	780
Qy	781	CTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCCCAAAGATCTCCCCAT	840
Db	781	CTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCCCAAAGATCTCCCCAT	840
Qy	841	TATGTTTGATGTCCTGATTCATGATCCTAGCCACTTCCTCAATTATTCTACCATTAACTA	900
Db	841	TATGTTTGATGTCCTGATTCATGATCCTAGCCACTTCCTCAATTATTCTACCATTAACTA	900
Qy	901	CAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTCACCAATCATACTGTGAATCA	960
Db	901	CAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTCACCAATCATACTGTGAATCA	960
Qy	961	CACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCAGG	1020
Db	961	CACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCAGG	1020
Qy	1021	ACCTTGTCGGCCACCGCCACCACCACCCAGACCTTCAAACCCACCCCTTCTTTAGGACC	1080
Db	1021	ACCTTGTCGGCCACCGCCACCACCACCCAGACCTTCAAACCCACCCCTTCTTTAGGACC	1080
Qy	1081	TGCTGGTGACAACCCCTGGAGCTGAGTAGGATTTCCTGATGAAAAGTCCAGATTAACAG	1140
Db	1081	TGCTGGTGACAACCCCTGGAGCTGAGTAGGATTTCCTGATGAAAAGTCCAGATTAACAG	1140
Qy	1141	ATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAGGTTAACATCAT	1200
Db	1141	ATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAGGTTAACATCAT	1200
Qy	1201	CCAGATGACAGACGTCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTTGT	1260
Db	1201	CCAGATGACAGACGTCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTTGT	1260
Qy	1261	CGTGACCTGCCAAGGGAGCATTCCACGGAGGTCTGTACCATCATTTCTGACCCACCTG	1320
Db	1261	CGTGACCTGCCAAGGGAGCATTCCACGGAGGTCTGTACCATCATTTCTGACCCACCTG	1320
Qy	1321	CGAGATCACCCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGATGTGTCTGCTGAC	1380
Db	1321	CGAGATCACCCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGATGTGTCTGCTGAC	1380
Qy	1381	TGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCTGGGGGATGA	1440
Db	1381	TGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCTGGGGGATGA	1440
Qy	1441	CACAAGCCTGGCTCTCACGAGCACCTGATTTCTGTTCTGACAGAGACCCAGCTCGCC	1500

Db	1441	 CACAAAGCCTGGCTCTCACGAGCACCTGATTTCTGTTCCCTGACAGAGACCCAGCCTCGCC	1500
Qy	1501	TTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACGTGT	1560
Db	1501	TTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACGTGT	1560
Qy	1561	GATCTCCCTCTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCTGG	1620
Db	1561	GATCTCCCTCTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCTGG	1620
Qy	1621	GAATGTGGTCAGAAGCAAAGGCCCTGAGTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTT	1680
Db	1621	GAATGTGGTCAGAAGCAAAGGCCCTGAGTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTT	1680
Qy	1681	CCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCTTA	1740
Db	1681	CCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCTTA	1740
Qy	1741	AATTTTCGACCTTGTCTTCTGAAGCTCACTTTTCAGTGCCATTGATGTGAGATGTGCTGGAG	1800
Db	1741	AATTTTCGACCTTGTCTTCTGAAGCTCACTTTTCAGTGCCATTGATGTGAGATGTGCTGGAG	1800
Qy	1801	TGGCTATTAACCTTTTTTTTCCCTAAAGATTATTGTTAAATAGATATTGTGGTTTGGGGAAG	1860
Db	1801	TGGCTATTAACCTTTTTTTTCCCTAAAGATTATTGTTAAATAGATATTGTGGTTTGGGGAAG	1860
Qy	1861	TTGAATTTTTTATAGGTTAAATGTCATTTTAGAGATGGGGAGAGGGATTATACTGCAGGC	1920
Db	1861	TTGAATTTTTTATAGGTTAAATGTCATTTTAGAGATGGGGAGAGGGATTATACTGCAGGC	1920
Qy	1921	AGCTTCAGCCATGTTGTGAAACTGATAAAAGCAACTTAGCAAGGCTTCTTTTCATTATTT	1980
Db	1921	AGCTTCAGCCATGTTGTGAAACTGATAAAAGCAACTTAGCAAGGCTTCTTTTCATTATTT	1980
Qy	1981	TTTATGTTTCACCTATAAAGTCTTAGGTAACCTAGTAGGATAGAAACACTGTGTCCCGAGA	2040
Db	1981	TTTATGTTTCACCTATAAAGTCTTAGGTAACCTAGTAGGATAGAAACACTGTGTCCCGAGA	2040
Qy	2041	GTAAGGAGAGAAGCTACTATTGATTAGAGCCTAACCCAGGTTAACTGCAAGAAGAGGCGG	2100
Db	2041	GTAAGGAGAGAAGCTACTATTGATTAGAGCCTAACCCAGGTTAACTGCAAGAAGAGGCGG	2100
Qy	2101	GATACTTTCAGCTTTCATGTAACCTGTATGCATAAAGCCAATGTAGTCCAGTTTCTAAGA	2160
Db	2101	GATACTTTCAGCTTTCATGTAACCTGTATGCATAAAGCCAATGTAGTCCAGTTTCTAAGA	2160
Qy	2161	TCATGTTCCAAGCTAACTGAATCCCACCTTCAATACACACTCATGAACCTCCTGATGGAACA	2220
Db	2161	TCATGTTCCAAGCTAACTGAATCCCACCTTCAATACACACTCATGAACCTCCTGATGGAACA	2220
Qy	2221	ATAACAGGCCCAAGCCTGTGGTATGATGTGCACACTTGCTAGACTCAGAAAAAATACTAC	2280
Db	2221	ATAACAGGCCCAAGCCTGTGGTATGATGTGCACACTTGCTAGACTCAGAAAAAATACTAC	2280
Qy	2281	TCTCATAAATGGGTGGGAGTATTTTGGTGACAACCTACTTTGCTTGGCTGAGTGAAGGAA	2340

Db	2281	TCTCATAAATGGGTGGGAGTATTTTGGTGACAACCTACTTTGCTTGGCTGAGTGAAGGAA	2340
Qy	2341	TGATATTCATATATTCATTTATTCATGGACATTTAGTTAGTGCCTTTTATATACCAGGC	2400
Db	2341	TGATATTCATATATTCATTTATTCATGGACATTTAGTTAGTGCCTTTTATATACCAGGC	2400
Qy	2401	ATGATGCTGAGTGACACTCTTGTGTATATTTCCAAATTTTGTATAGTCGCTGCACATAT	2460
Db	2401	ATGATGCTGAGTGACACTCTTGTGTATATTTCCAAATTTTGTATAGTCGCTGCACATAT	2460
Qy	2461	TTGAAATCAAAATATTAAGACTTTCCAAAAATTTGGTCCCTGGTTTTTCATGGCAACTTG	2520
Db	2461	TTGAAATCAAAATATTAAGACTTTCCAAAAATTTGGTCCCTGGTTTTTCATGGCAACTTG	2520
Qy	2521	ATCAGTAAGGATTTCCCCTCTGTTTGGAACTAAAACCATTTACTATATGTTAGACAAGAC	2580
Db	2521	ATCAGTAAGGATTTCCCCTCTGTTTGGAACTAAAACCATTTACTATATGTTAGACAAGAC	2580
Qy	2581	ATTTTTTTTTTTTTCCTTCCTGAAAAAAAAATGAGGGAAGAGACAAAAAAAAAAAAAAAA	2640
Db	2581	ATTTTTTTTTTTTTCCTTCCTGAAAAAAAAATGAGGGAAGAGACAAAAAAAAAAAAAAAA	2640
Qy	2641	AAAAAAAAAAAAAAAAAAAAA	2661
Db	2641	AAAAAAAAAAAAAAAAAAAAA	2661

RESULT 2

ADQ22838

ID ADQ22838 standard; DNA; 2845 BP.

XX

AC ADQ22838;

XX

DT 26-AUG-2004 (first entry)

XX

DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5658.

XX

KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW ds.

XX

OS Homo sapiens.

XX

PN WO2004048938-A2.

XX

PD 10-JUN-2004.

XX

PF 26-NOV-2003; 2003WO-US038193.

XX

PR 26-NOV-2002; 2002US-0429739P.

XX

PA (PROT-) PROTEIN DESIGN LABS INC.

XX

PI Aziz N, Ginsburg WM, Zlotnik A;

XX

DR WPI; 2004-441208/41.

XX

PT Early detection of soft tissue sarcoma comprises determining expression

Qy	508	AAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCCGGATGGAGAA	567
Db	620	AAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCCGGATGGAGAA	679
Qy	568	GATGGAATTTTCATCTACGTCTTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGAT	627
Db	680	GATGGAATTTTCATCTACGTCTTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGAT	739
Qy	628	GTTTCAGTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAG	687
Db	740	GTTTCAGTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAG	799
Qy	688	TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAAGTGAAAGATGTGT	747
Db	800	TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAAGTGAAAGATGTGT	859
Qy	748	ACGTGGTAACAGATCAGATTCCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATT	807
Db	860	ACGTGGTAACAGATCAGATTCCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATT	919
Qy	808	CATCCGACGAAACCTTCC-CAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC	866
Db	920	CATCCGACGAAACCTTCCCTCAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC	979
Qy	867	CTAGCCACTTCCTCAATTATTCTACCATTAACACAAGTGGAGCTTCGGGGATAAATACTG	926
Db	980	CTAGCCACTTCCTCAATTATTCTACCATTAACACAAGTGGAGCTTCGGGGATAAATACTG	1039
Qy	927	GCCTGTTTGTTCACCAATCATACTGTGAATCACACGTATGTGCTCAATGGAACCTTCA	986
Db	1040	GCCTGTTTGTTCACCAATCATACTGTGAATCACACGTATGTGCTCAATGGAACCTTCA	1099
Qy	987	GCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCCGCCACCGCCACCACCAC	1046
Db	1100	GCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCCGCCACCGCCACCACCAC	1159
Qy	1047	CCAGACCTTCAAAACCCACCCCTTCTTTAGGACCTGCTGGTGACAACCCCTGGAGCTGA	1106
Db	1160	CCAGACCTTCAAAACCCACCCCTTCTTTAGGACCTGCTGGTGACAACCCCTGGAGCTGA	1219
Qy	1107	GTAGGATTCCTGATGAAAACCTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCA	1166
Db	1220	GTAGGATTCCTGATGAAAACCTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCA	1279
Qy	1167	CAATTGTAGAGGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGTCTTGATGCCGG	1226
Db	1280	CAATTGTAGAGGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGTCTTGATGCCGG	1339
Qy	1227	TGCCATGGCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATTTCCA	1286
Db	1340	TGCCATGGCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATTTCCA	1399
Qy	1287	CGGAGGTCTGTACCATCATTTCTGACCCACCTGCGAGATCACCCAGAACACAGTCTGCA	1346
Db	1400	CGGAGGTCTGTACCATCATTTCTGACCCACCTGCGAGATCACCCAGAACACAGTCTGCA	1459

Qy	1347	GCCCTGTGGATGTGGATGAGATGTGTCTGCTGACTGTGAGACGAACCTTCAATGGGTCTG	1406
Db	1460	GCCCTGTGGATGTGGATGAGATGTGTCTGCTGACTGTGAGACGAACCTTCAATGGGTCTG	1519
Qy	1407	GGACGTAAGTGTGAACCTCACCTGGGGGATGACACAAGCCTGGCTCTCACGAGCACCC	1466
Db	1520	GGACGTAAGTGTGAACCTCACCTGGGGGATGACACAAGCCTGGCTCTCACGAGCACCC	1579
Qy	1467	TGATTTCTGTTCCCTGACAGAGACCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGA	1526
Db	1580	TGATTTCTGTTCCCTGACAGAGACCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGA	1639
Qy	1527	TCTCCGTTGGCTGCTTGGCCATATTTGTCACTGTGATCTCCCTCTTGGTGTACAAAAAC	1586
Db	1640	TCTCCGTTGGCTGCTTGGCCATATTTGTCACTGTGATCTCCCTCTTGGTGTACAAAAAC	1699
Qy	1587	ACAAGGAATACAACCCAATAGAAAATAGTCCTGGGAATGTGGTCAGAAGCAAAGGCCCTGA	1646
Db	1700	ACAAGGAATACAACCCAATAGAAAATAGTCCTGGGAATGTGGTCAGAAGCAAAGGCCCTGA	1759
Qy	1647	GTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTTCCCGGAAACCAGGAAAAGGATCCGC	1706
Db	1760	GTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTTCCCGGAAACCAGGAAAAGGATCCGC	1819
Qy	1707	TACTCAAAAACCAAGAATTTAAAGGAGTTTCTTAAATTTTCGACCTTGTTTCTGAAGCTCA	1766
Db	1820	TACTCAAAAACCAAGAATTTAAAGGAGTTTCTTAAATTTTCGACCTTGTTTCTGAAGCTCA	1879
Qy	1767	CTTTTCAGTGCCATTGATGTGAGATGTGCTGGAGTGGCTATTAACCTTTTTTTCCTAAAG	1826
Db	1880	CTTTTCAGTGCCATTGATGTGAGATGTGCTGGAGTGGCTATTAACCTTTTTTTCCTAAAG	1939
Qy	1827	ATTATTGTTAAATAGATATTGTGGTTTGGGGAAGTTGAATTTTTTATAGGTTAAATGTCA	1886
Db	1940	ATTATTGTTAAATAGATATTGTGGTTTGGGGAAGTTGAATTTTTTATAGGTTAAATGTCA	1999
Qy	1887	TTTTAGAGATGGGGAGAGGGATTATACTGCAGGCAGCTTCAGCCATGTTGTGAAACTGAT	1946
Db	2000	TTTTAGAGATGGGGAGAGGGATTATACTGCAGGCAGCTTCAGCCATGTTGTGAAACTGAT	2059
Qy	1947	AAAAGCAACTTAGCAAGGCTTCTTTTCATTATTTTTTATGTTTCACCTTATAAAGTCTTAG	2006
Db	2060	AAAAGCAACTTAGCAAGGCTTCTTTTCATTATTTTTTATGTTTCACCTTATAAAGTCTTAG	2119
Qy	2007	GTAAC TAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAGAAGCTACTATTGATTA	2066
Db	2120	GTAAC TAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAGAAGCTACTATTGATTA	2179
Qy	2067	GAGCCTAACCCAGGTTAACTGCAAGAAGAGGCGGGATACTTTCAGCTTTCATGTAACCTG	2126
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Qy	2127	TATGCATAAAGCCAATGTAGTCCAGTTTCTAAGATCATGTTCCAAGCTAACTGAATCCCA	2186
Db	2240	TATGCATAAAGCCAATGTAGTCCAGTTTCTAAGATCATGTTCCAAGCTAACTGAATCCCA	2299
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Db      2300 CTTCAATACACACTCATGAACCTCTGATGGAACAATAACAGGCCCAAGCCTGTGGTATGA 2359
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Qy      2307 GTGACAACCTACTTTGCTTGGCTGAGTGAAGGAATGATATTCATATATTCATTTATTCCA 2366
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GenCore version 5.1.6
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(without alignments)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	2547.8	95.7	2669	1	US-08-594-031-101	Sequence 101, App
7	1664.6	62.6	1683	4	US-09-943-075A-8	Sequence 8, Appli
8	1051.2	39.5	2303	4	US-09-197-970B-4	Sequence 4, Appli
9	1047.8	39.4	2213	3	US-09-383-586-27	Sequence 27, Appl
10	1047.8	39.4	2213	4	US-09-823-038A-27	Sequence 27, Appl
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41	480.8	18.1	698	3	US-09-643-597-5	Sequence 5, Appli
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ALIGNMENTS

RESULT 1

US-09-985-799-91

; Sequence 91, Application US/09985799

; Patent No. RE38392

; GENERAL INFORMATION:

; APPLICANT: THOMPSON, Timothy C.

; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES

; NUMBER OF SEQUENCES: 175

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BAKER & BOTTS, L.L.P.

; STREET: 1299 Pennsylvania Avenue, N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20004-2400

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/985,799

; FILING DATE: 06-No. RE38392-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/594,031

; FILING DATE: 30-JAN-1996

; APPLICATION NUMBER: 60/006,838

; FILING DATE: 16-NOV-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Remenick, James

; REGISTRATION NUMBER: 36,902

; REFERENCE/DOCKET NUMBER: 0A146-0110

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-639-7700

; TELEFAX: 202-639-7890

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 91:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2669 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

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;      ANTI-SENSE: NO
;      FRAGMENT TYPE: <Unknown>
;      ORIGINAL SOURCE:
;      SEQUENCE DESCRIPTION: SEQ ID NO: 91:
US-09-985-799-91
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Db	120	TTCTGCTCCTGGCTGCAAGATTGCCACTTGATGCCGCCAAACGATTTTCATGATGTGCTGG	179
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Qy	328	TGGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAAGGAAGATG	387
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2571.2	96.6	2845	18	US-10-723-860-5658	Sequence 5658, Ap
4	2559.2	96.2	2952	14	US-10-198-846-10843	Sequence 10843, A
5	2547.8	95.7	2669	10	US-09-525-978B-82	Sequence 82, Appl
6	2547.8	95.7	2669	17	US-10-172-118-779	Sequence 779, App
7	2547.8	95.7	2669	17	US-10-295-027-1041	Sequence 1041, Ap
8	2547.8	95.7	2669	17	US-10-342-887-779	Sequence 779, App
9	2547.8	95.7	2669	18	US-10-450-826-92	Sequence 92, Appl
10	2547.8	95.7	2669	18	US-10-723-860-1127	Sequence 1127, Ap
11	2531.6	95.1	2666	15	US-10-084-817-169	Sequence 169, App
12	2485	93.4	2683	14	US-10-227-884-41	Sequence 41, Appl
13	2485	93.4	2683	14	US-10-230-163-41	Sequence 41, Appl
14	2485	93.4	2683	14	US-10-230-338-41	Sequence 41, Appl
15	2485	93.4	2683	14	US-10-218-631-41	Sequence 41, Appl
16	2485	93.4	2683	14	US-10-230-414-41	Sequence 41, Appl
17	2485	93.4	2683	14	US-10-232-224-41	Sequence 41, Appl
18	2485	93.4	2683	14	US-10-216-159A-41	Sequence 41, Appl
19	2485	93.4	2683	14	US-10-218-849-41	Sequence 41, Appl
20	2485	93.4	2683	14	US-10-227-873-41	Sequence 41, Appl
21	2485	93.4	2683	14	US-10-227-883-41	Sequence 41, Appl
22	2485	93.4	2683	14	US-10-219-076-41	Sequence 41, Appl
23	2485	93.4	2683	14	US-10-230-434-41	Sequence 41, Appl
24	2485	93.4	2683	14	US-10-219-003-41	Sequence 41, Appl
25	2485	93.4	2683	14	US-10-219-075-41	Sequence 41, Appl
26	2485	93.4	2683	14	US-10-219-464-41	Sequence 41, Appl
27	2485	93.4	2683	14	US-10-219-466-41	Sequence 41, Appl
28	2485	93.4	2683	14	US-10-219-479-41	Sequence 41, Appl
29	2485	93.4	2683	14	US-10-219-481-41	Sequence 41, Appl
30	2485	93.4	2683	14	US-10-230-260-41	Sequence 41, Appl
31	2485	93.4	2683	14	US-10-232-231-41	Sequence 41, Appl
32	2485	93.4	2683	14	US-10-232-233-41	Sequence 41, Appl
33	2485	93.4	2683	14	US-10-216-165-41	Sequence 41, Appl
34	2485	93.4	2683	14	US-10-218-956-41	Sequence 41, Appl
35	2485	93.4	2683	14	US-10-219-468-41	Sequence 41, Appl
36	2485	93.4	2683	14	US-10-219-478-41	Sequence 41, Appl
37	2485	93.4	2683	14	US-10-219-536-41	Sequence 41, Appl

ALIGNMENTS

```

; Sequence 1, Application US/10039272
; Publication No. US20020168653A1
; GENERAL INFORMATION:
;   APPLICANT: RAMESHWAR, Pranela
;   TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTOR INDUCIBLE NEUROKININ-TYPE
;   FILE REFERENCE: 267/033 University of Medicine & Dentistry of New Jersey
;   CURRENT APPLICATION NUMBER: US/10/039,272
;   CURRENT FILING DATE: 2001-10-20
;   PRIOR APPLICATION NUMBER: US 60/241,881
;   PRIOR FILING DATE: 2000-10-20
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 2661
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-039-272-1

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Query Match 100.0%; Score 2661; DB 13; Length 2661;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2661; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CGGCACGAGGGCCCAGAGGAATAAGTTAACCTTGGTGCCTGCGTCCGTGAGAATTCAGCA	60
Db	1	CGGCACGAGGGCCCAGAGGAATAAGTTAACCTTGGTGCCTGCGTCCGTGAGAATTCAGCA	60
Qy	61	TGGAATGTCTCTACTATTTCTGGGATTTCTGCTCCTGGCTGCAAGATTGCCACTTGATG	120
Db	61	TGGAATGTCTCTACTATTTCTGGGATTTCTGCTCCTGGCTGCAAGATTGCCACTTGATG	120
Qy	121	CCGCCAAACGATTTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAGC	180
Db	121	CCGCCAAACGATTTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAGC	180
Qy	181	ACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAACTCTACCCAG	240
Db	181	ACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAACTCTACCCAG	240
Qy	241	TGTGGAAGCGGGGAGACATGAGGTGGAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGG	300
Db	241	TGTGGAAGCGGGGAGACATGAGGTGGAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGG	300

Qy	301	TCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTGA	360
Db	301	TCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTGA	360
Qy	361	TATTCCTTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAACTGCA	420
Db	361	TATTCCTTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAACTGCA	420
Qy	421	GAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAACCTGGACAGCATGGTCAGAGG	480
Db	421	GAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAACCTGGACAGCATGGTCAGAGG	480
Qy	481	ACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAAC	540
Db	481	ACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAAC	540
Qy	541	CTTTTCCTCACCACCCCGGATGGAGAAGATGGAATTTTCATCTACGTCTTCCACACACTTG	600
Db	541	CTTTTCCTCACCACCCCGGATGGAGAAGATGGAATTTTCATCTACGTCTTCCACACACTTG	600
Qy	601	GTCAGTATTTCCAGAAATTGGGACGATGTTTCAGTGAGAGTTTCTGTGAACACAGCCAATG	660
Db	601	GTCAGTATTTCCAGAAATTGGGACGATGTTTCAGTGAGAGTTTCTGTGAACACAGCCAATG	660
Qy	661	TGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATG	720
Db	661	TGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATG	720
Qy	721	TTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTGA	780
Db	721	TTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTGA	780
Qy	781	CTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCCCAAAGATCTCCCCAT	840
Db	781	CTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCCCAAAGATCTCCCCAT	840
Qy	841	TATGTTTGATGTCCTGATTGATCCTAGCCACTTCCTCAATTATTCTACCATTAACTA	900
Db	841	TATGTTTGATGTCCTGATTGATCCTAGCCACTTCCTCAATTATTCTACCATTAACTA	900
Qy	901	CAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATACTGTGAATCA	960
Db	901	CAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATACTGTGAATCA	960
Qy	961	CACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCAGG	1020
Db	961	CACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCAGG	1020
Qy	1021	ACCTTGTCGGCCACCGCCACCACCACCCAGACCTTCAAACCCACCCCTTCTTTAGGACC	1080
Db	1021	ACCTTGTCGGCCACCGCCACCACCACCCAGACCTTCAAACCCACCCCTTCTTTAGGACC	1080
Qy	1081	TGCTGGTGACAACCCCTGGAGCTGAGTAGGATTTCCTGATGAAAACCTGCCAGATTAAACAG	1140
Db	1081	TGCTGGTGACAACCCCTGGAGCTGAGTAGGATTTCCTGATGAAAACCTGCCAGATTAAACAG	1140
Qy	1141	ATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAGGTTAACATCAT	1200

Db	1141	 ATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAGGTTAACATCAT	1200
Qy	1201	CCAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTTGT	1260
Db	1201	CCAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTTGT	1260
Qy	1261	CGTGACCTGCCAAGGGAGCATTCCACGGAGGTCTGTACCATCATTTCTGACCCACCTG	1320
Db	1261	CGTGACCTGCCAAGGGAGCATTCCACGGAGGTCTGTACCATCATTTCTGACCCACCTG	1320
Qy	1321	CGAGATCACCCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGATGTGTCTGCTGAC	1380
Db	1321	CGAGATCACCCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGATGTGTCTGCTGAC	1380
Qy	1381	TGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCTGGGGGATGA	1440
Db	1381	TGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCTGGGGGATGA	1440
Qy	1441	CACAAGCCTGGCTCTCACGAGCACCTGATTTCTGTTCCCTGACAGAGACCCAGCCTCGCC	1500
Db	1441	CACAAGCCTGGCTCTCACGAGCACCTGATTTCTGTTCCCTGACAGAGACCCAGCCTCGCC	1500
Qy	1501	TTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACTGT	1560
Db	1501	TTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACTGT	1560
Qy	1561	GATCTCCCTCTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCTGG	1620
Db	1561	GATCTCCCTCTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCTGG	1620
Qy	1621	GAATGTGGTCAGAAGCAAAGGCCTGAGTGTCTTTCTCAACCGTGCAAAGCCGTGTTCTT	1680
Db	1621	GAATGTGGTCAGAAGCAAAGGCCTGAGTGTCTTTCTCAACCGTGCAAAGCCGTGTTCTT	1680
Qy	1681	CCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCTTA	1740
Db	1681	CCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCTTA	1740
Qy	1741	AATTTTCGACCTTGTCTTCTGAAGCTCACTTTTCAGTGCCATTGATGTGAGATGTGCTGGAG	1800
Db	1741	AATTTTCGACCTTGTCTTCTGAAGCTCACTTTTCAGTGCCATTGATGTGAGATGTGCTGGAG	1800
Qy	1801	TGGCTATTAACCTTTTTTTCCTAAAGATTATTGTTAAATAGATATTGTGGTTTGGGGAAG	1860
Db	1801	TGGCTATTAACCTTTTTTTCCTAAAGATTATTGTTAAATAGATATTGTGGTTTGGGGAAG	1860
Qy	1861	TTGAATTTTTTATAGGTTAAATGTCATTTTAGAGATGGGGAGAGGGATTATACTGCAGGC	1920
Db	1861	TTGAATTTTTTATAGGTTAAATGTCATTTTAGAGATGGGGAGAGGGATTATACTGCAGGC	1920
Qy	1921	AGCTTCAGCCATGTTGTGAAACTGATAAAAGCAACTTAGCAAGGCTTCTTTTCATTATTT	1980
Db	1921	AGCTTCAGCCATGTTGTGAAACTGATAAAAGCAACTTAGCAAGGCTTCTTTTCATTATTT	1980
Qy	1981	TTTATGTTTCACCTATAAAGTCTTAGGTAAGTAGTAGGATAGAAACACTGTGTCCCGAGA	2040

Db 1981 TTTATGTTTCAC TTATAAAGTCTTAGGTAAGTAGTAGGATAGAAACACTGTGTCCCGAGA 2040
 Qy 2041 GTAAGGAGAGAAGCTACTATTGATTAGAGCCTAACCCAGGTAACTGCAAGAAGAGGCGG 2100
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 Db 2041 GTAAGGAGAGAAGCTACTATTGATTAGAGCCTAACCCAGGTAACTGCAAGAAGAGGCGG 2100
 Qy 2101 GATACTTTCAGCTTTCCATGTAAGTGTATGCATAAAGCCAATGTAGTCCAGTTTCTAAGA 2160
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 Db 2101 GATACTTTCAGCTTTCCATGTAAGTGTATGCATAAAGCCAATGTAGTCCAGTTTCTAAGA 2160
 Qy 2161 TCATGTTCCAAGCTAACTGAATCCCACCTTCAATACACACTCATGAACTCCTGATGGAACA 2220
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 Db 2161 TCATGTTCCAAGCTAACTGAATCCCACCTTCAATACACACTCATGAACTCCTGATGGAACA 2220
 Qy 2221 ATAACAGGCCCAAGCCTGTGGTATGATGTGCACACTTGCTAGACTCAGAAAAAATACTAC 2280
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 Db 2221 ATAACAGGCCCAAGCCTGTGGTATGATGTGCACACTTGCTAGACTCAGAAAAAATACTAC 2280
 Qy 2281 TCTCATAAATGGGTGGGAGTATTTTGGTGACAACCTACTTTGCTTGGCTGAGTGAAGGAA 2340
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 Db 2281 TCTCATAAATGGGTGGGAGTATTTTGGTGACAACCTACTTTGCTTGGCTGAGTGAAGGAA 2340
 Qy 2341 TGATATTCATATATTCATTTATTCATGGACATTTAGTTAGTGCCTTTTATATACCAGGC 2400
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 Db 2341 TGATATTCATATATTCATTTATTCATGGACATTTAGTTAGTGCCTTTTATATACCAGGC 2400
 Qy 2401 ATGATGCTGAGTGACACTCTTGTGTATATTTCCAAATTTTGTATAGTCGCTGCACATAT 2460
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 Db 2401 ATGATGCTGAGTGACACTCTTGTGTATATTTCCAAATTTTGTATAGTCGCTGCACATAT 2460
 Qy 2461 TTGAAATCAAAATATTAAGACTTTCCAAAAATTTGGTCCCTGGTTTTTTCATGGCAACTTG 2520
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 Db 2461 TTGAAATCAAAATATTAAGACTTTCCAAAAATTTGGTCCCTGGTTTTTTCATGGCAACTTG 2520
 Qy 2521 ATCAGTAAGGATTTCCCCTCTGTTTGGAACATAAACCATTACTATATGTTAGACAAGAC 2580
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 Db 2521 ATCAGTAAGGATTTCCCCTCTGTTTGGAACATAAACCATTACTATATGTTAGACAAGAC 2580
 Qy 2581 ATTTTTTTTTTTTTTCCCTTCTGAAAAAAAAAATGAGGGAAGAGACAAAAAAAAAAAAAAAAA 2640
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 Db 2581 ATTTTTTTTTTTTTTCCCTTCTGAAAAAAAAAATGAGGGAAGAGACAAAAAAAAAAAAAAAAA 2640
 Qy 2641 AAAAAAAAAAAAAAAAAAAAAA 2661
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 Db 2641 AAAAAAAAAAAAAAAAAAAAAA 2661

RESULT 2

US-10-463-106-1

; Sequence 1, Application US/10463106

; Publication No. US20030202938A1

; GENERAL INFORMATION:

; APPLICANT: RAMESHWAR, Pranela

; TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTOR INDUCIBLE NEUROKININ-1 GENE

; FILE REFERENCE: 267/033 University of Medicine & Dentistry of New Jersey

; CURRENT APPLICATION NUMBER: US/10/463,106

; CURRENT FILING DATE: 2003-06-17

; PRIOR APPLICATION NUMBER: US 10/039,272
; PRIOR FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/241,881
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2661
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-463-106-1

Query Match 100.0%; Score 2661; DB 17; Length 2661;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2661; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CGGCACGAGGGCCAGAGGAATAAGTTAACCTTGGTGCCTGCGTCCGTGAGAATTCAGCA	60
Db	1	CGGCACGAGGGCCAGAGGAATAAGTTAACCTTGGTGCCTGCGTCCGTGAGAATTCAGCA	60
Qy	61	TGGAATGTCTCTACTATTTCTGGGATTTCTGCTCCTGGCTGCAAGATTGCCACTTGATG	120
Db	61	TGGAATGTCTCTACTATTTCTGGGATTTCTGCTCCTGGCTGCAAGATTGCCACTTGATG	120
Qy	121	CCGCCAAACGATTTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAGC	180
Db	121	CCGCCAAACGATTTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAGC	180
Qy	181	ACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAACTCTACCCAG	240
Db	181	ACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAACTCTACCCAG	240
Qy	241	TGTGGAAGCGGGGAGACATGAGGTGGAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGG	300
Db	241	TGTGGAAGCGGGGAGACATGAGGTGGAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGG	300
Qy	301	TCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTGA	360
Db	301	TCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTGA	360
Qy	361	TATTCCCTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAAGCTGCA	420
Db	361	TATTCCCTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAAGCTGCA	420
Qy	421	GAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAACCTGGACAGCATGGTCAGAGG	480
Db	421	GAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAACCTGGACAGCATGGTCAGAGG	480
Qy	481	ACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAAC	540
Db	481	ACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAAC	540
Qy	541	CTTTTCCTCACCACCCCGGATGGAGAAGATGGAATTTTCATCTACGTCTTCCACACACTTG	600
Db	541	CTTTTCCTCACCACCCCGGATGGAGAAGATGGAATTTTCATCTACGTCTTCCACACACTTG	600
Qy	601	GTCAGTATTTCCAGAAATTGGGACGATGTTTCAGTGAGAGTTTCTGTGAACACAGCCAATG	660

Db	601	 GTCAGTATTTCCAGAAATTGGGACGATGTTTCAGTGAGAGTTTCTGTGAACACAGCCAATG	660
Qy	661	TGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATG	720
Db	661	 TGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATG	720
Qy	721	TTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTGA	780
Db	721	 TTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTGA	780
Qy	781	CTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCCCAAAGATCTCCCCAT	840
Db	781	 CTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCCCAAAGATCTCCCCAT	840
Qy	841	TATGTTTGATGTCCTGATTGATCCTAGCCACTTCCTCAATTATTCTACCATTAACATA	900
Db	841	 TATGTTTGATGTCCTGATTGATCCTAGCCACTTCCTCAATTATTCTACCATTAACATA	900
Qy	901	CAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTCACCAATCATACTGTGAATCA	960
Db	901	 CAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTCACCAATCATACTGTGAATCA	960
Qy	961	CACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCAGG	1020
Db	961	 CACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCAGG	1020
Qy	1021	ACCTTGTCGGCCACCGCCACCACCACCCAGACCTTCAAACCCACCCCTTCTTTAGGACC	1080
Db	1021	 ACCTTGTCGGCCACCGCCACCACCACCACCCAGACCTTCAAACCCACCCCTTCTTTAGGACC	1080
Qy	1081	TGCTGGTGACAACCCCTGGAGCTGAGTAGGATTCTGATGAAAACCTGCCAGATTAACAG	1140
Db	1081	 TGCTGGTGACAACCCCTGGAGCTGAGTAGGATTCTGATGAAAACCTGCCAGATTAACAG	1140
Qy	1141	ATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAGGTTAACATCAT	1200
Db	1141	 ATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAGGTTAACATCAT	1200
Qy	1201	CCAGATGACAGACGTCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTTGT	1260
Db	1201	 CCAGATGACAGACGTCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTTGT	1260
Qy	1261	CGTGACCTGCCAAGGGAGCATTTCCACGGAGGTCTGTACCATCATTTCTGACCCACCTG	1320
Db	1261	 CGTGACCTGCCAAGGGAGCATTTCCACGGAGGTCTGTACCATCATTTCTGACCCACCTG	1320
Qy	1321	CGAGATCACCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGATGTGTCTGCTGAC	1380
Db	1321	 CGAGATCACCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGATGTGTCTGCTGAC	1380
Qy	1381	TGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCTGGGGGATGA	1440
Db	1381	 TGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCTGGGGGATGA	1440
Qy	1441	CACAAGCCTGGCTCTCACGAGCACCCTGATTTCTGTTCCCTGACAGAGACCCAGCCTCGCC	1500

Db	1441	CACAAGCCTGGCTCTCACGAGCACCTGATTTCTGTTCTGACAGAGACCCAGCCTCGCC	1500
Qy	1501	TTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACTGT	1560
Db	1501	TTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACTGT	1560
Qy	1561	GATCTCCCTCTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAAAATAGTCCTGG	1620
Db	1561	GATCTCCCTCTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAAAATAGTCCTGG	1620
Qy	1621	GAATGTGGTCAGAAGCAAAGGCCTGAGTGTCTTTCTCAACCGTGCAAAGCCGTGTTCTT	1680
Db	1621	GAATGTGGTCAGAAGCAAAGGCCTGAGTGTCTTTCTCAACCGTGCAAAGCCGTGTTCTT	1680
Qy	1681	CCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCTTA	1740
Db	1681	CCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCTTA	1740
Qy	1741	AATTTTCGACCTTGTTTCTGAAGCTCACTTTTCAGTGCCATTGATGTGAGATGTGCTGGAG	1800
Db	1741	AATTTTCGACCTTGTTTCTGAAGCTCACTTTTCAGTGCCATTGATGTGAGATGTGCTGGAG	1800
Qy	1801	TGGCTATTAACCTTTTTTTTCCCTAAAGATTATTGTTAAATAGATATTGTGGTTTGGGGAAG	1860
Db	1801	TGGCTATTAACCTTTTTTTTCCCTAAAGATTATTGTTAAATAGATATTGTGGTTTGGGGAAG	1860
Qy	1861	TTGAATTTTTTATAGGTTAAATGTCATTTTAGAGATGGGGAGAGGGATTATACTGCAGGC	1920
Db	1861	TTGAATTTTTTATAGGTTAAATGTCATTTTAGAGATGGGGAGAGGGATTATACTGCAGGC	1920
Qy	1921	AGCTTCAGCCATGTTGTGAAACTGATAAAAGCAACTTAGCAAGGCTTCTTTTCATTATTT	1980
Db	1921	AGCTTCAGCCATGTTGTGAAACTGATAAAAGCAACTTAGCAAGGCTTCTTTTCATTATTT	1980
Qy	1981	TTTATGTTTCACTTATAAAGTCTTAGGTAAGTAGTAGGATAGAAACACTGTGTCCCGAGA	2040
Db	1981	TTTATGTTTCACTTATAAAGTCTTAGGTAAGTAGTAGGATAGAAACACTGTGTCCCGAGA	2040
Qy	2041	GTAAGGAGAGAAGCTACTATTGATTAGAGCCTAACCCAGGTAACTGCAAGAAGAGGCGG	2100
Db	2041	GTAAGGAGAGAAGCTACTATTGATTAGAGCCTAACCCAGGTAACTGCAAGAAGAGGCGG	2100
Qy	2101	GATACTTTCAGCTTTCATGTAAGTGTATGCATAAAGCCAATGTAGTCCAGTTTCTAAGA	2160
Db	2101	GATACTTTCAGCTTTCATGTAAGTGTATGCATAAAGCCAATGTAGTCCAGTTTCTAAGA	2160
Qy	2161	TCATGTTCCAAGCTAACTGAATCCCACTTCAATACACACTCATGAACCTCCTGATGGAACA	2220
Db	2161	TCATGTTCCAAGCTAACTGAATCCCACTTCAATACACACTCATGAACCTCCTGATGGAACA	2220
Qy	2221	ATAACAGGCCCAAGCCTGTGGTATGATGTGCACACTTGCTAGACTCAGAAAAAATACTAC	2280
Db	2221	ATAACAGGCCCAAGCCTGTGGTATGATGTGCACACTTGCTAGACTCAGAAAAAATACTAC	2280
Qy	2281	TCTCATAAATGGGTGGGAGTATTTTGGTGACAACCTACTTTGCTTGGCTGAGTGAAGGAA	2340
Db	2281	TCTCATAAATGGGTGGGAGTATTTTGGTGACAACCTACTTTGCTTGGCTGAGTGAAGGAA	2340

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Qy      2341 TGATATTCATATATTCATTTATTCATGGACATTTAGTTAGTGCTTTTATATACCAGGC 2400
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Db      2341 TGATATTCATATATTCATTTATTCATGGACATTTAGTTAGTGCTTTTATATACCAGGC 2400

Qy      2401 ATGATGCTGAGTGACACTCTTGTGTATATTTCCAAATTTTGTATAGTCGCTGCACATAT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 ATGATGCTGAGTGACACTCTTGTGTATATTTCCAAATTTTGTATAGTCGCTGCACATAT 2460

Qy      2461 TTGAAATCAAAATATTAAGACTTTCCAAAAATTTGGTCCCTGGTTTTTCATGGCAACTTG 2520
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Db      2461 TTGAAATCAAAATATTAAGACTTTCCAAAAATTTGGTCCCTGGTTTTTCATGGCAACTTG 2520

Qy      2521 ATCAGTAAGGATTTCCCCTCTGTTTGGAACTAAAACCATTACTATATGTTAGACAAGAC 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 ATCAGTAAGGATTTCCCCTCTGTTTGGAACTAAAACCATTACTATATGTTAGACAAGAC 2580

Qy      2581 ATTTTTTTTTTTTTTCCTTCCTGAAAAAAAAATGAGGGAAGAGACAAAAAAAAAAAAAAAA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 ATTTTTTTTTTTTTTCCTTCCTGAAAAAAAAATGAGGGAAGAGACAAAAAAAAAAAAAAAA 2640

Qy      2641 AAAAAAAAAAAAAAAAAAAAAAA 2661
          ||||||||||||||||
Db      2641 AAAAAAAAAAAAAAAAAAAAAAA 2661

```

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2005, 10:29:04 ; Search time 7723 Seconds
(without alignments)
13115.243 Million cell updates/sec

Title: US-10-039-272-1
Perfect score: 2661
Sequence: 1 cggcacgagggcccagagga.....aaaaaaaaaaaaaaaaaaaaa 2661

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*

3: gb_hlc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB		ID	Description
No.	Score	Match	Length	DB	ID			
1	2550	95.8	2636	3	BC025297			BC025297 Homo sapi
2	1698	63.8	1757	3	CR620418			CR620418 full-leng
3	1664.8	62.6	1695	3	CR625459			CR625459 full-leng
4	1617	60.8	1726	3	CR626032			CR626032 full-leng
5	1049.8	39.5	3615	3	AK044764			AK044764 Mus muscu
6	1046.6	39.3	2265	3	AK076347			AK076347 Mus muscu
c 7	1017.4	38.2	1106	5	BX397314			BX397314 BX397314
c 8	1013.6	38.1	1050	5	BX379978			BX379978 BX379978
9	943.8	35.5	2431	3	AK079220			AK079220 Mus muscu
c 10	932.6	35.0	971	5	BX423077			BX423077 BX423077
c 11	926.6	34.8	1015	5	BX458448			BX458448 BX458448
12	918	34.5	1029	5	BX406949			BX406949 BX406949
13	913.6	34.3	998	5	BX379979			BX379979 BX379979
14	910.6	34.2	1063	5	BX336884			BX336884 BX336884
15	906.4	34.1	1067	5	BX364871			BX364871 BX364871
16	885.6	33.3	947	5	BX458449			BX458449 BX458449
17	867.4	32.6	895	7	CF552020			CF552020 AGENCOURT
18	864.4	32.5	949	5	BX423078			BX423078 BX423078
c 19	863.4	32.4	1011	5	BX406948			BX406948 BX406948
c 20	862.2	32.4	905	1	AL542811			AL542811 AL542811
c 21	851.2	32.0	930	5	BX364870			BX364870 BX364870
22	844.6	31.7	987	5	BX381217			BX381217 BX381217
c 23	835.4	31.4	1035	1	AL575920			AL575920 AL575920
c 24	827.2	31.1	957	5	BX396828			BX396828 BX396828
25	823	30.9	858	1	AL542812			AL542812 AL542812
26	816.6	30.7	891	5	BX452668			BX452668 BX452668
27	815.8	30.7	911	4	BI521316			BI521316 603081887
28	799.8	30.1	910	5	BX396829			BX396829 BX396829
29	796.8	29.9	858	4	BG742951			BG742951 602632050
30	788	29.6	1107	4	BM550298			BM550298 AGENCOURT
31	779	29.3	1089	4	BM547872			BM547872 AGENCOURT
32	776	29.2	835	4	BG576651			BG576651 602597538
33	775	29.1	808	4	BG742272			BG742272 602631402
34	775	29.1	962	4	BG676576			BG676576 602623049
35	758.2	28.5	810	1	AU139997			AU139997 AU139997
c 36	749.8	28.2	993	1	AL564958			AL564958 AL564958
37	745	28.0	754	4	BG211992			BG211992 RST31703
38	743.8	28.0	892	5	BU157659			BU157659 AGENCOURT
c 39	742.4	27.9	878	5	BX437190			BX437190 BX437190
40	737.8	27.7	855	5	BU178305			BU178305 AGENCOURT

41	733.8	27.6	807	4	BG696053	BG696053	602658007
42	731.6	27.5	905	6	CD109017	CD109017	AGENCOURT
43	728.2	27.4	857	5	BU150501	BU150501	AGENCOURT
44	722.2	27.1	808	6	CD108927	CD108927	AGENCOURT
c 45	715.2	26.9	894	1	AL550419	AL550419	AL550419

ALIGNMENTS

RESULT 1

BC025297

LOCUS BC025297 2636 bp mRNA linear HTC 08-MAR-2002

DEFINITION Homo sapiens, glycoprotein (transmembrane) nmb, clone
IMAGE:4877773, mRNA.

ACCESSION BC025297

VERSION BC025297.1 GI:19264140

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2636)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (05-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 42 Row: i Column: 5

This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4505404

This clone has the following problem: frame shifted.

FEATURES

source

Location/Qualifiers

1. .2636

/organism="Homo sapiens"

/mol_type="mRNA"

Qy	688	TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAGATGTGT	747
Db	680	TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAGATGTGT	739
Qy	748	ACGTGGTAACAGATCAGATTCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATT	807
Db	740	ACGTGGTAACAGATCAGATTCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATT	799
Qy	808	CATCCGACGAAACCTTCC-CAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC	866
Db	800	CATCCGACGAAACCTTCCTCAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC	859
Qy	867	CTAGCCACTTCCTCAATTATTCTACCATTAACACAAGTGGAGCTTCGGGGATAAATACTG	926
Db	860	CTAGCCACTTCCTCAATTATTCTACCATTAACACAAGTGGAGCTTCGGGGATAAATACTG	919
Qy	927	GCCTGTTTGTTCACCAATCATACTGTGAATCACACGTATGTGCTCAATGGAACCTTCA	986
Db	920	GCCTGTTTGTTCACCAATCATACTGTGAATCACACGTATGTGCTCAATGGAACCTTCA	979
Qy	987	GCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCGCCACCGCCACCACCAC	1046
Db	980	GCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCGCCACCGCCACCACCAC	1039
Qy	1047	CCAGACCTTCAAACCCACCCCTTCTTTAGGACCTGCTGGTGACAACCCCTGGAGCTGA	1106
Db	1040	CCAGACCTTCAAACCCACCCCTTCTTTAGGACCTGCTGGTGACAACCCCTGGAGCTGA	1099
Qy	1107	GTAGGATTCCTGATGAAAACCTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCA	1166
Db	1100	GTAGGATTCCTGATGAAAACCTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCA	1159
Qy	1167	CAATTGTAGAGGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGTCTGATGCCGG	1226
Db	1160	CAATTGTAGAGGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGTCTGATGCCGG	1219
Qy	1227	TGCCATGGCCTGAAAGCTCCCTAATAGACTTTGTCTGACCTGCCAAGGGAGCATTCCCA	1286
Db	1220	TGCCATGGCCTGAAAGCTCCCTAATAGACTTTGTCTGACCTGCCAAGGGAGCATTCCCA	1279
Qy	1287	CGGAGGTCTGTACCATCATTTCTGACCCACCTGCGAGATCACCCAGAACACAGTCTGCA	1346
Db	1280	CGGAGGTCTGTACCATCATTTCTGACCCACCTGCGAGATCACCCAGAACACAGTCTGCA	1339
Qy	1347	GCCCTGTGGATGTGGATGAGATGTGTCTGCTGACTGTGAGACGAACCTTCAATGGGTCTG	1406
Db	1340	GCCCTGTGGATGTGGATGAGATGTGTCTGCTGACTGTGAGACGAACCTTCAATGGGTCTG	1399
Qy	1407	GGACGTACTGTGTGAACCTCACCTGGGGGATGACACAAGCCTGGCTCTCACGAGCACCC	1466
Db	1400	GGACGTACTGTGTGAACCTCACCTGGGGGATGACACAAGCCTGGCTCTCACGAGCACCC	1459
Qy	1467	TGATTTCTGTTCTGACAGAGACCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGA	1526
Db	1460	TGATTTCTGTTCTGACAGAGACCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGA	1519
Qy	1527	TCTCCGTTGGCTGCTTGGCCATATTTGTCACTGTGATCTCCCTCTTGGTGTACAAAAAAC	1586

Db	1520	TCTCCGTTGGCTGCTTGGCCATATTTGTCACGTGTGATCTCCCTCTTGGTGTACAAAAAAC	1579
Qy	1587	ACAAGGAATACAACCCAATAGAAAATAGTCCTGGGAATGTGGTCAGAAGCAAAGGCCTGA	1646
Db	1580	ACAAGGAATACAACCCAATAGAAAATAGTCCTGGGAATGTGGTCAGAAGCAAAGGCCTGA	1639
Qy	1647	GTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTTCCCGGGAAACCAGGAAAAGGATCCGC	1706
Db	1640	GTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTTCCCGGGAAACCAGGAAAAGGATCCGC	1699
Qy	1707	TACTCAAAAACCAAGAATTTAAAGGAGTTTCTTAAATTTTCGACCTTGTTTCTGAAGCTCA	1766
Db	1700	TACTCAAAAACCAAGAATTTAAAGGAGTTTCTTAAATTTTCGACCTTGTTTCTGAAGCTCA	1759
Qy	1767	CTTTTCAGTGCCATTGATGTGAGATGTGCTGGAGTGGCTATTAACCTTTTTTTCCTAAAG	1826
Db	1760	CTTTTCAGTGCCATTGATGTGAGATGTGCTGGAGTGGCTATTAACCTTTTTTTCCTAAAG	1819
Qy	1827	ATTATTGTTAAATAGATATTGTGGTTTGGGGAAGTTGAATTTTTTATAGGTTAAATGTCA	1886
Db	1820	ATTATTGTTAAATAGATATTGTGGTTTGGGGAAGTTGAATTTTTTATAGGTTAAATGTCA	1879
Qy	1887	TTTTAGAGATGGGGAGAGGGATTATACTGCAGGCAGCTTCAGCCATGTTGTGAAACTGAT	1946
Db	1880	TTTTAGAGATGGGGAGAGGGATTATACTGCAGGCAGCTTCAGCCATGTTGTGAAACTGAT	1939
Qy	1947	AAAAGCAACTTAGCAAGGCTTCTTTTCATTATTTTTTATGTTTCACCTATAAAGTCTTAG	2006
Db	1940	AAAAGCAACTTAGCAAGGCTTCTTTTCATTATTTTTTATGTTTCACCTATAAAGTCTTAG	1999
Qy	2007	GTAAC TAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAGAAGCTACTATTGATTA	2066
Db	2000	GTAAC TAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAGAAGCTACTATTGATTA	2059
Qy	2067	GAGCCTAACCCAGGTAACTGCAAGAAGAGGCGGGATACTTTCAGCTTTCATGTAAGT	2126
Db	2060	GAGCCTAACCCAGGTAACTGCAAGAAGAGGCGGGATACTTTCAGCTTTCATGTAAGT	2119
Qy	2127	TATGCATAAAGCCAATGTAGTCCAGTTTCTAAGATCATGTTCCAAGCTAACTGAATCCCA	2186
Db	2120	TATGCATAAAGCCAATGTAGTCCAGTTTCTAAGATCATGTTCCAAGCTAACTGAATCCCA	2179
Qy	2187	CTTCAATACACACTCATGAACTCCTGATGGAACAATAACAGGCCCAAGCCTGTGGTATGA	2246
Db	2180	CTTCAATACACACTCATGAACTCCTGATGGAACAATAACAGGCCCAAGCCTGTGGTATGA	2239
Qy	2247	TGTGCACACTTGCTAGACTCAGAAAAAATACTACTCTCATAAATGGGTGGGAGTATTTTG	2306
Db	2240	TGTGCACACTTGCTAGACTCAGAAAAAATACTACTCTCATAAATGGGTGGGAGTATTTTG	2299
Qy	2307	GTGACAACCTACTTTGCTTGGCTGAGTGAAGGAATGATATTCATATATTCATTTATTCCA	2366
Db	2300	GTGACAACCTACTTTGCTTGGCTGAGTGAAGGAATGATATTCATATATTCATTTATTCCA	2359
Qy	2367	TGGACATTTAGTTAGTGCTTTTTTATATACCAGGCATGATGCTGAGTGACACTCTTGTGTA	2426

Db 2360 TGGACATTTAGTTAGTGCTTTTTATATACCAGGCATGATGCTGAGTGACACTCTTGTGTA 2419

Qy 2427 TATTTCCAAATTTTTGTATAGTCGCTGCACATATTTGAAATCAAATATTAAGACTTTCC 2486
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Db 2420 TATTTCCAAATTTTTGTACAGTCGCTGCACATATTTGAAATC-ATATATTAAGACTTTCC 2478

Qy 2487 AAAAATTTGGTCCCTGGTTTTTCATGGCAACTTGATCAGTAAGGATTTCCCCTCTGTTTG 2546
||| || |||||

Db 2479 AAAGATGAGGTCCCTGGTTTTTCATGGCAACTTGATCAGTAAGGATTTACCTCTGTTTG 2538

Qy 2547 GAACTAAAACCATTTACTATATGTTAGACAAGACATTTTTTTTTTTTCCCTTCCTGAAAAA 2606
|||||

Db 2539 TAACTAAAACCATCTACTATATGTTAGACATGACATTCTTTTTCTCTCCTTCCTGAAAAA 2598

Qy 2607 -AAAATGAGGGAAGAGACAAAAAAAAAAAAAAAAAAAA 2643
||| || |||||

Db 2599 TAAAGTGTGGGAAGAGACAAAAAAAAAAAAAAAAAAAA 2636

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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 18, 2005, 22:03:33 ; Search time 355 Seconds
(without alignments)
5798.137 Million cell updates/sec

Title: US-10-039-272-1
Perfect score: 4850
Sequence: 1 cggcacgagggccagagga.....aaaaaaaaaaaaaaaaaaaaa 2661

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlp

-
Q=/cgn2_1/USPTO_spool_p/US10039272/runat_18022005_095204_14690/app_query.fasta_1
.2823

-DB=A_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10039272_CGN_1_1_398@runat_18022005_095204_14690 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	3014	62.1	563	8	ADR66659	Adr66659	Human pro
2	3014	62.1	563	8	ADR66317	Adr66317	Human pro
3	3014	62.1	563	8	ADR66339	Adr66339	Human pro
4	3014	62.1	563	8	ADR66681	Adr66681	Human pro
5	2999	61.8	560	2	AAW35382	Aaw35382	Murine me
6	2999	61.8	560	3	AAB11329	Aab11329	Human lun
7	2999	61.8	560	5	ABB78200	Abb78200	Amino aci
8	2999	61.8	560	5	ABB74961	Abb74961	Human lun
9	2999	61.8	560	5	ABP61881	Abp61881	Human lun
10	2999	61.8	560	6	ABU56592	Abu56592	Lung canc
11	2999	61.8	560	6	ABG72962	Abg72962	Human ost
12	2999	61.8	560	6	ABU70852	Abu70852	Human adi
13	2999	61.8	560	7	ADA28315	Ada28315	Human lun
14	2999	61.8	560	7	ADE95620	Ade95620	Human NOV
15	2999	61.8	560	7	ADH36879	Adh36879	Human lun
16	2999	61.8	560	7	ADJ68660	Adj68660	Human hea
17	2999	61.8	560	7	ADL14995	Adl14995	Human NMB
18	2999	61.8	560	7	ADN39940	Adn39940	Cancer/an
19	2999	61.8	560	8	ADH56342	Adh56342	Human nmb
20	2999	61.8	560	8	ADJ75569	Adj75569	Marker ge
21	2999	61.8	560	8	ADM56682	Adm56682	Human lun
22	2999	61.8	560	8	ADQ18310	Adq18310	Human sof
23	2999	61.8	560	8	ADP23127	Adp23127	PRO polyp
24	2980	61.4	572	7	ADD78235	Add78235	Human CGD
25	2979	61.4	572	5	AAU83612	Aau83612	Human PRO
26	2979	61.4	572	6	ABU80759	Abu80759	Human PRO
27	2979	61.4	572	6	ABO33725	Abo33725	Novel hum
28	2979	61.4	572	6	ABU82068	Abu82068	Novel hum
29	2979	61.4	572	6	ABJ72248	Abj72248	Human PRO
30	2979	61.4	572	6	ABJ72376	Abj72376	Human PRO
31	2979	61.4	572	6	ABO34271	Abo34271	Human sec
32	2979	61.4	572	7	ABJ72078	Abj72078	Human mem
33	2979	61.4	572	7	ADB83532	Adb83532	Novel hum
34	2979	61.4	572	7	ADB80638	Adb80638	Novel hum
35	2979	61.4	572	7	ADB73179	Adb73179	Novel hum
36	2979	61.4	572	7	ADB78261	Adb78261	Novel hum
37	2979	61.4	572	7	ADB84909	Adb84909	Human PRO
38	2979	61.4	572	7	ADB78015	Adb78015	Novel hum
39	2979	61.4	572	7	ADB87081	Adb87081	Human PRO
40	2979	61.4	572	7	ADB84663	Adb84663	Human PRO
41	2979	61.4	572	7	ADB83778	Adb83778	Novel hum
42	2979	61.4	572	7	ADB72933	Adb72933	Novel hum
43	2979	61.4	572	7	ADC36771	Adc36771	Human PRO
44	2979	61.4	572	7	ADC21761	Adc21761	Human PRO
45	2979	61.4	572	7	ADC49792	Adc49792	Novel hum

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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 18, 2005, 22:15:00 ; Search time 73 Seconds
(without alignments)
5442.224 Million cell updates/sec

Title: US-10-039-272-1
Perfect score: 4850
Sequence: 1 cggcacgagggccagagga.....aaaaaaaaaaaaaaaaaaaaa 2661

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10039272/runat_18022005_095206_14721/app_query.fasta_1
.2823

-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10039272_CGN_1_1_72_runat_18022005_095206_14721 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	2999	61.8	560	1	US-09-985-799-90	Sequence 90, Appl	
2	2999	61.8	560	1	US-09-977-371-90	Sequence 90, Appl	
3	2999	61.8	560	1	US-08-594-031-90	Sequence 90, Appl	
4	2999	61.8	560	4	US-09-643-597-225	Sequence 225, App	
5	2999	61.8	560	4	US-09-480-884A-225	Sequence 225, App	
6	2999	61.8	560	4	US-09-542-615A-225	Sequence 225, App	
7	2999	61.8	560	4	US-09-606-421B-225	Sequence 225, App	
8	2999	61.8	560	4	US-09-476-496A-225	Sequence 225, App	
9	2999	61.8	560	4	US-09-630-940B-225	Sequence 225, App	
10	2999	61.8	560	4	US-09-943-075A-6	Sequence 6, Appli	
11	2170	44.7	574	3	US-09-383-586-36	Sequence 36, Appl	
12	2170	44.7	574	4	US-09-823-038A-36	Sequence 36, Appl	
13	2170	44.7	574	4	US-09-943-075A-5	Sequence 5, Appli	
14	2152	44.4	572	4	US-09-197-970B-5	Sequence 5, Appli	
15	2136	44.0	572	4	US-09-943-075A-2	Sequence 2, Appli	
16	950.5	19.6	376	1	US-09-985-799-100	Sequence 100, App	
17	950.5	19.6	376	1	US-09-985-799-102	Sequence 102, App	
18	950.5	19.6	376	1	US-09-977-371-100	Sequence 100, App	
19	950.5	19.6	376	1	US-09-977-371-102	Sequence 102, App	
20	950.5	19.6	376	1	US-08-594-031-100	Sequence 100, App	
21	950.5	19.6	376	1	US-08-594-031-102	Sequence 102, App	
22	593	12.2	661	2	US-08-417-174-121	Sequence 121, App	
23	593	12.2	661	3	US-09-267-439-121	Sequence 121, App	
24	593	12.2	661	4	US-08-388-852B-2	Sequence 2, Appli	
25	593	12.2	661	4	US-09-073-138-121	Sequence 121, App	
26	592	12.2	661	2	US-08-417-174-27	Sequence 27, Appl	
27	592	12.2	661	2	US-08-231-565A-27	Sequence 27, Appl	
28	592	12.2	661	2	US-09-007-961-27	Sequence 27, Appl	
29	592	12.2	661	3	US-09-267-439-27	Sequence 27, Appl	
30	592	12.2	661	4	US-09-073-138-27	Sequence 27, Appl	
31	574.5	11.8	668	1	US-07-891-942G-6	Sequence 6, Appli	
32	327.5	6.8	460	4	US-09-949-016-8029	Sequence 8029, Ap	
33	238.5	4.9	190	4	US-08-388-852B-35	Sequence 35, Appl	
34	236	4.9	202	4	US-08-388-852B-38	Sequence 38, Appl	
35	233.5	4.8	192	4	US-08-388-852B-37	Sequence 37, Appl	
36	233	4.8	197	4	US-08-388-852B-36	Sequence 36, Appl	
37	124	2.6	71	1	US-09-985-799-98	Sequence 98, Appl	
38	124	2.6	71	1	US-09-977-371-98	Sequence 98, Appl	
39	124	2.6	71	1	US-08-594-031-98	Sequence 98, Appl	
40	120	2.5	724	4	US-09-784-358-8	Sequence 8, Appli	
41	120	2.5	845	4	US-09-784-358-12	Sequence 12, Appl	
42	120	2.5	1691	4	US-09-784-358-2	Sequence 2, Appli	
43	112.5	2.3	440	4	US-09-248-796A-26860	Sequence 26860, A	
44	111	2.3	525	4	US-09-976-594-64	Sequence 64, Appl	
45	111	2.3	525	4	US-09-919-039-62	Sequence 62, Appl	

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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 18, 2005, 22:44:56 ; Search time 303.5 Seconds
(without alignments)
5738.309 Million cell updates/sec

Title: US-10-039-272-1
Perfect score: 4850
Sequence: 1 cggcacgagggccagagga.....aaaaaaaaaaaaaaaaaaaaa 2661

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 2760536

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10039272/runat_18022005_095208_14781/app_query.fasta_1
.2823

-DB=Published_Applications_AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10039272_@CGN_1_1_393_@runat_18022005_095208_14781
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	2999	61.8	560	9	US-09-735-705-225	Sequence 225, App
2	2999	61.8	560	9	US-09-850-716A-225	Sequence 225, App
3	2999	61.8	560	9	US-09-897-778-225	Sequence 225, App
4	2999	61.8	560	9	US-09-943-075A-6	Sequence 6, Appli
5	2999	61.8	560	13	US-10-039-272-2	Sequence 2, Appli
6	2999	61.8	560	14	US-10-007-700-225	Sequence 225, App
7	2999	61.8	560	14	US-10-117-982-225	Sequence 225, App
8	2999	61.8	560	15	US-10-463-106-2	Sequence 2, Appli
9	2999	61.8	560	15	US-10-295-027-1258	Sequence 1258, Ap
10	2999	61.8	560	15	US-10-313-986-225	Sequence 225, App
11	2999	61.8	560	15	US-10-309-290-152	Sequence 152, App
12	2999	61.8	560	16	US-10-408-765A-466	Sequence 466, App
13	2979	61.4	572	14	US-10-227-884-42	Sequence 42, Appl
14	2979	61.4	572	14	US-10-230-163-42	Sequence 42, Appl
15	2979	61.4	572	14	US-10-230-338-42	Sequence 42, Appl
16	2979	61.4	572	14	US-10-218-631-42	Sequence 42, Appl
17	2979	61.4	572	14	US-10-230-414-42	Sequence 42, Appl
18	2979	61.4	572	14	US-10-232-224-42	Sequence 42, Appl
19	2979	61.4	572	14	US-10-216-159A-42	Sequence 42, Appl
20	2979	61.4	572	14	US-10-218-849-42	Sequence 42, Appl
21	2979	61.4	572	14	US-10-227-873-42	Sequence 42, Appl
22	2979	61.4	572	14	US-10-227-883-42	Sequence 42, Appl
23	2979	61.4	572	14	US-10-219-076-42	Sequence 42, Appl
24	2979	61.4	572	14	US-10-230-434-42	Sequence 42, Appl
25	2979	61.4	572	14	US-10-219-003-42	Sequence 42, Appl
26	2979	61.4	572	14	US-10-219-075-42	Sequence 42, Appl
27	2979	61.4	572	14	US-10-219-464-42	Sequence 42, Appl
28	2979	61.4	572	14	US-10-219-466-42	Sequence 42, Appl
29	2979	61.4	572	14	US-10-219-479-42	Sequence 42, Appl
30	2979	61.4	572	14	US-10-219-481-42	Sequence 42, Appl
31	2979	61.4	572	14	US-10-230-260-42	Sequence 42, Appl
32	2979	61.4	572	14	US-10-232-231-42	Sequence 42, Appl
33	2979	61.4	572	14	US-10-232-233-42	Sequence 42, Appl
34	2979	61.4	572	14	US-10-216-165-42	Sequence 42, Appl
35	2979	61.4	572	14	US-10-218-956-42	Sequence 42, Appl
36	2979	61.4	572	14	US-10-219-468-42	Sequence 42, Appl
37	2979	61.4	572	14	US-10-219-478-42	Sequence 42, Appl
38	2979	61.4	572	14	US-10-219-536-42	Sequence 42, Appl
39	2979	61.4	572	14	US-10-233-205-42	Sequence 42, Appl
40	2979	61.4	572	14	US-10-219-072-42	Sequence 42, Appl
41	2979	61.4	572	14	US-10-219-470-42	Sequence 42, Appl
42	2979	61.4	572	14	US-10-219-474-42	Sequence 42, Appl
43	2979	61.4	572	14	US-10-219-524-42	Sequence 42, Appl

44	2979	61.4	572	14	US-10-219-528-42	Sequence 42, Appl
45	2979	61.4	572	14	US-10-227-880-42	Sequence 42, Appl

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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 18, 2005, 22:06:53 ; Search time 91 Seconds
(without alignments)
5627.095 Million cell updates/sec

Title: US-10-039-272-1
Perfect score: 4850
Sequence: 1 cggcacgagggcccagagga.....aaaaaaaaaaaaaaaaaaaaa 2661

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10039272/runat_18022005_095205_14708/app_query.fasta_1
.2823

-DB=PIR_79 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10039272_@CGN_1_1_135_@runat_18022005_095205_14708 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB	ID	Description
No.	Score	Match	Length				
1	2999	61.8	560	2	I38065		gene NMB protein -
2	635	13.1	626	2	S53871		Pmel 17 protein -
3	593.5	12.2	662	2	I38400		melanoma-associate
4	588.5	12.1	668	2	A41234		melanocyte-specifi
5	436.5	9.0	491	2	A49179		melanoma antigen h
6	135	2.8	446	2	T07907		hydroxyproline-ric
7	129	2.7	926	1	A41105		protein-tyrosine-p
8	118	2.4	2869	2	T18518		apolipoprotein(a)
9	116.5	2.4	555	2	S21766		dihydrolipoamide S
10	114	2.4	2395	1	S50820		surface protein ty
11	113	2.3	1541	2	T02831		AAA protein L4171.
12	112.5	2.3	457	2	I55976		dihydrolipoamide S
13	111.5	2.3	2946	2	T15840		hypothetical prote
14	111	2.3	525	1	KGHUGH		histidine-rich gly
15	110.5	2.3	1874	1	JQ0533		genome polyprotein
16	109.5	2.3	492	2	C96521		protein F21D18.18
17	109	2.2	1737	2	A59235		unconventional myo
18	108.5	2.2	348	2	AB3260		hypothetical membr
19	108.5	2.2	588	2	T45564		hypothetical prote
20	107.5	2.2	768	2	A87722		protein ZC123.1 [i
21	107.5	2.2	1208	2	T27822		hypothetical prote
22	106	2.2	658	2	T08153		cysteine proteinas
23	106	2.2	1537	2	S53465		flocculation prote
24	106	2.2	1585	2	T31611		hypothetical prote
c 25	105	2.2	499	2	S52422		chitinase (EC 3.2.
26	104.5	2.2	4006	2	T09070		probable tenascin
27	104	2.1	435	2	D41602		transcription fact
28	103	2.1	626	1	NBHUIA		platelet glycoprot
29	103	2.1	921	2	A33718		retinoblastoma pro
30	103	2.1	1009	2	C64483		hypothetical prote
c 31	102.5	2.1	394	2	E82572		ABC transporter so
32	102.5	2.1	826	2	G90283		hypothetical prote
33	102.5	2.1	979	2	A35913		regulatory factor
34	102	2.1	281	2	T29150		hypothetical prote
35	102	2.1	393	2	T33103		lin-1 protein - Ca
36	102	2.1	1213	2	A41724		limb deformity (ld
37	102	2.1	2014	2	T21560		hypothetical prote
38	101.5	2.1	445	2	D81716		hypothetical prote
39	101.5	2.1	2165	2	T21371		hypothetical prote
40	101	2.1	848	2	T23694		hypothetical prote
41	101	2.1	2090	2	S26058		probable transform
42	100.5	2.1	221	2	T07176		extensin homolog -
43	100.5	2.1	1048	2	T30815		platelet-derived g
44	100	2.1	432	2	AB2222		twitching motility
45	100	2.1	26926	1	I38344		titin, cardiac mus

OM nucleic - protein search, using frame plus n2p model

```
Run on:      February 18, 2005, 22:04:28 ; Search time 445 Seconds
              (without alignments)
              6124.237 Million cell updates/sec
```

Title: US-10-039-272-1
Perfect score: 4850
Sequence: 1 cggcacgagggcccgagga.....aaaaaaaaaaaaaaaaaaaaa 2661

```
Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop  6.0 , Delext 7.0
```

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Command line parameters:

```
-MODEL=frame+ n2p.model -DEV=xlp
```

Q=/cgn2_1/USPTO_spool_p/US10039272/runat_18022005_095205_14696/app_query.fasta_1.2823

```
-DB=UniProt_03 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10039272_CGN_1_1_518@runat_18022005_095205_14696 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

```
Database :      UniProt_03:*
              1:  uniprot_sprot:*
              2:  uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%						
Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	2999	61.8	560	1	NMB_HUMAN	Q14956	homo sapien
2	2983	61.5	572	2	Q8N1A1	Q8n1a1	homo sapien
3	2979	61.4	572	2	Q6UVX1	Q6uvx1	homo sapien
4	2170	44.7	574	2	Q99P91	Q99p91	mus musculu
5	2170	44.7	574	2	Q8BVV9	Q8bvv9	mus musculu
6	2170	44.7	574	2	Q9QXA0	Q9qxa0	mus musculu
7	2166	44.7	574	2	Q8BXL4	Q8bxl4	mus musculu
8	2152	44.4	572	2	Q6P7C7	Q6p7c7	rattus norv
9	2136	44.0	572	2	Q9QZF6	Q9qzf6	rattus norv
10	2015	41.5	526	2	Q8BVA0	Q8bva0	mus musculu
11	1563.5	32.2	559	1	QNR_COTJA	Q90372	coturnix co
12	1029	21.2	206	2	Q96F58	Q96f58	homo sapien
13	1022	21.1	206	2	Q8IXJ5	Q8ixj5	homo sapien
14	711.5	14.7	721	2	Q6DDN6	Q6ddn6	xenopus lae
15	704.5	14.5	746	2	Q6DIR2	Q6dir2	xenopus tro
16	644.5	13.3	626	2	Q9CZB2	Q9czb2	mus musculu
17	635	13.1	626	1	PM17_MOUSE	Q60696	mus musculu
18	631.5	13.0	760	2	Q6DW64	Q6dw64	gallus gall
19	630	13.0	733	2	O93391	O93391	coturnix co
20	629.5	13.0	764	2	Q6DW63	Q6dw63	gallus gall
21	628	12.9	763	2	Q6DW62	Q6dw62	gallus gall
22	620.5	12.8	788	2	Q6DW65	Q6dw65	gallus gall
23	617	12.7	762	1	P115_CHICK	Q98917	gallus gall
24	612	12.6	783	2	Q6DW60	Q6dw60	gallus gall
25	609	12.6	759	2	Q6DW61	Q6dw61	gallus gall
26	593	12.2	661	1	PM17_HUMAN	P40967	homo sapien
27	436.5	9.0	491	1	PM17_BOVIN	Q06154	bos taurus
28	372	7.7	461	2	O97884	O97884	equus cabal
29	247.5	5.1	236	2	Q9QY67	Q9qy67	mus musculu
30	198.5	4.1	423	2	Q8NOW9	Q8n0w9	homo sapien
31	198.5	4.1	435	2	Q8N3G9	Q8n3g9	homo sapien
32	192	4.0	397	2	Q8N3R2	Q8n3r2	homo sapien
33	167	3.4	141	2	Q9QY70	Q9qy70	mus musculu
34	154.5	3.2	419	2	Q6NXM3	Q6nxm3	mus musculu
35	151	3.1	354	2	Q8IY46	Q8iy46	homo sapien
36	141.5	2.9	906	2	Q8TPY9	Q8tpy9	methanosarc
37	135	2.8	446	2	O22458	O22458	chlamydomon
38	134.5	2.8	1817	2	Q8TI59	Q8ti59	methanosarc
39	131	2.7	879	2	Q8PWJ6	Q8pwj6	methanosarc
40	129.5	2.7	1131	2	Q75DJ5	Q75dj5	ashbya goss
41	129	2.7	926	1	PTN4_HUMAN	P29074	homo sapien
42	128.5	2.6	688	2	Q8TR88	Q8tr88	methanosarc
43	127.5	2.6	3988	2	Q8TPZ1	Q8tpz1	methanosarc
44	126	2.6	603	2	Q7U5X8	Q7u5x8	synechococc
45	125.5	2.6	881	2	Q6H7U3	Q6h7u3	oryza sativ